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SEQUENCE LISTING

<110> TANABE SEIYAKU CO., LTD.

<120> Three-dimensional structure of dipeptidyl peptidase IV

<130> 03-039-PCT

<150> US 60/398,761

<151> 2002-07-29

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 2301

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(2301)

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 1 5 10 15
 ctt gtc acc atc atc acc gtg ccc gig gtt ctg ctg aac aaa ggc aca 96
 Leu Val Thr Ile Ile Thr Val Pro Val Val Leu Leu Asn Lys Gly Thr
 20 25 30
 gat gat gct aca gct gac agt cgc aaa act tac act cta act gat tac 144
 Asp Asp Ala Thr Ala Asp Ser Arg Lys Thr Tyr Thr Leu Thr Asp Tyr
 35 40 45
 tta aaa aat act tat aga ctg aag tta tac tcc tta aga tgg att tca 192
 Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr Ser Leu Arg Trp Ile Ser
 50 55 60
 gat cat gaa tat ctc tac aaa caa gaa aat aat atc ttg gta ttc aat 240
 Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn Asn Ile Leu Val Phe Asn
 65 70 75 80
 gct gaa tat gga aac agc tca gtt ttc ttg gag aac agt aca ttt gat 288
 Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu Glu Asn Ser Thr Phe Asp
 85 90 95
 gag ttt gga cat tct atc aat gat tat tca ata tct cct gat ggg cag 336
 Glu Phe Gly His Ser Ile Asn Asp Tyr Ser Ile Ser Pro Asp Gly Gln
 100 105 110
 ttt att ctc tta gaa tac aac tac gtg aag caa tgg agg cat tcc tac 384
 Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys Gln Trp Arg His Ser Tyr
 115 120 125
 aca gct tca tat gac att tat gat tta aat aaa agg cag ctg att aca 432
 Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn Lys Arg Gln Leu Ile Thr
 130 135 140
 gaa gag agg att cca aac aac aca cag tgg gtc aca tgg tca cca gtg 480

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Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp Val Thr Trp Ser Pro Val
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Gly His Lys Leu Ala Tyr Val Trp Asn Asn Asp Ile Tyr Val Lys Ile
165 170 175
gaa cca aat tta cca agt tac aga atc aca tgg acg ggg aaa gaa gat 576
Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr Trp Thr Gly Lys Glu Asp
180 185 190
ata ata tat aat gga ata act gac tgg gtt tat gaa gag gaa gtc ttc 624
Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val Tyr Glu Glu Val Phe
195 200 205
agt gcc tac tct gct ctg tgg tgg tct cca aac ggc act ttt tia gca 672
Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro Asn Gly Thr Phe Leu Ala
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tat gcc caa ttt aac gac aca gaa gtc cca ctt att gaa tac tcc ttc 720
Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro Leu Ile Glu Tyr Ser Phe
225 230 235 240
tac tct gat gag tca ctg cag tac cca aag act gta cgg gtt cca tat 768
Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys Thr Val Arg Val Pro Tyr
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cca aag gca gga gct gtg aat cca act gta aag ttc ttt gtt gta aat 816
Pro Lys Ala Gly Ala Val Asn Pro Thr Val Lys Phe Phe Val Val Asn
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Thr Asp Ser Leu Ser Ser Val Thr Asn Ala Thr Ser Ile Gln Ile Thr
275 280 285
gct cct gct tct atg ttg ata ggg gat cac tac ttg tgt gat gtg aca 912

Ala Pro Ala Ser Met Leu Ile Gly Asp His Tyr Leu Cys Asp Val Thr
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 Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln Trp Leu Arg Arg Ile Gln
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 aac tat tcg gtc atg gat att tgt gac tat gat gaa tcc agt gga aga 1008
 Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr Asp Glu Ser Ser Gly Arg
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 340 345 350
 tgg gtt gga aga ttt agg cct tca gaa cct cat ttt acc ctt gat ggt 1104
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 Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys Thr Phe Ile Thr Lys Gly
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 Thr Trp Glu Val Ile Gly Ile Glu Ala Leu Thr Ser Asp Tyr Leu Tyr
 405 410 415
 tac att agt aat gaa tat aaa gga atg cca gga gga agg aat ctt tat 1296
 Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro Gly Gly Arg Asn Leu Tyr
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 aaa atc caa ctt agt gac tat aca aaa gtg aca tgc ctc agt tgt gag 1344

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Lys Ile Gln Leu Ser Asp Tyr Thr Lys Val Thr Cys Leu Ser Cys Glu
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 ctg aat ccg gaa agg tgt cag tac tat tct gtg tca ttc agt aaa gag 1392
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 Thr Leu His Ser Ser Val Asn Asp Lys Gly Leu Arg Val Leu Glu Asp
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 Asn Ser Ala Leu Asp Lys Met Leu Gln Asn Val Gln Met Pro Ser Lys
 500 505 510
 aaa ctg gac ttc att att ttg aat gaa aca aaa ttt tgg tat cag atg 1584
 Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr Lys Phe Trp Tyr Gln Met
 515 520 525
 atc ttg cct cct cat ttt gat aaa tcc aag aaa tat cct cta cta tta 1632
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 Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys Ala Asp Thr Val Phe Arg
 545 550 555 560
 ctg aac tgg gcc act tac ctt gca agc aca gaa aac att ata gta gct 1728
 Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr Glu Asn Ile Ile Val Ala
 565 570 575
 agc ttt gat ggc aga gga agt ggt tac caa gga gat aag atc atg cat 1776

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Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln Gly Asp Lys Ile Met His
580 585 590
gca atc aac aga aga ctg gga aca ttt gaa gtt gaa gat caa att gaa 1824
Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu Val Glu Asp Gln Ile Glu
595 600 605
gca gcc aga caa ttt tca aaa atg gga ttt gtg gac aac aaa cga att 1872
Ala Ala Arg Gln Phe Ser Lys Met Gly Phe Val Asp Asn Lys Arg Ile
610 615 620
gca att tgg ggc tgg tca tat gga ggg tac gta acc tca atg gtc ctg 1920
Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Thr Ser Met Val Leu
625 630 635 640
gga tcg gga agt ggc gtg ttc aag tgt gga ata gcc gtg gcg cct gta 1968
Gly Ser Gly Ser Gly Val Phe Lys Cys Gly Ile Ala Val Ala Pro Val
645 650 655
tcc cgg tgg gag tac tat gac tca gtg tac aca gaa cgt tac atg ggt 2016
Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr Thr Glu Arg Tyr Met Gly
660 665 670
ctc cca act cca gaa gac aac ctt gac cat tac aga aat tca aca gtc 2064
Leu Pro Thr Pro Glu Asp Asn Leu Asp His Tyr Arg Asn Ser Thr Val
675 680 685
atg agc aga gct gaa aat ttt aaa caa gtt gag tac ctc ctt att cat 2112
Met Ser Arg Ala Glu Asn Phe Lys Gln Val Glu Tyr Leu Leu Ile His
690 695 700
gga aca gca gat gat aac gtt cac ttt cag cag tca gct cag atc tcc 2160
Gly Thr Ala Asp Asp Asn Val His Phe Gln Gln Ser Ala Gln Ile Ser
705 710 715 720
aaa gcc ctg gtc gat gtt gga gtg gat ttc cag gca atg tgg tat act 2208

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Lys Ala Leu Val Asp Val Gly Val Asp Phe Gln Ala Met Trp Tyr Thr

725

730

735

gat gaa gac cat gga ata gct agc agc aca gca cac caa cat ata tat 2256

Asp Glu Asp His Gly Ile Ala Ser Ser Thr Ala His Gln His Ile Tyr

740

745

750

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755

760

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25

30

Asp Asp Ala Thr Ala Asp Ser Arg Lys Thr Tyr Thr Leu Thr Asp Tyr

35

40

45

Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr Ser Leu Arg Trp Ile Ser

50

55

60

Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn Asn Ile Leu Val Phe Asn

65

70

75

80

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Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu Glu Asn Ser Thr Phe Asp
85 90 95

Glu Phe Gly His Ser Ile Asn Asp Tyr Ser Ile Ser Pro Asp Gly Gln
100 105 110

Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys Gln Trp Arg His Ser Tyr
115 120 125

Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn Lys Arg Gln Leu Ile Thr
130 135 140

Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp Val Thr Trp Ser Pro Val
145 150 155 160

Gly His Lys Leu Ala Tyr Val Trp Asn Asn Asp Ile Tyr Val Lys Ile
165 170 175

Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr Trp Thr Gly Lys Glu Asp
180 185 190

Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val Tyr Glu Glu Glu Val Phe
195 200 205

Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro Asn Gly Thr Phe Leu Ala
210 215 220

Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro Leu Ile Glu Tyr Ser Phe
225 230 235 240

Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys Thr Val Arg Val Pro Tyr
245 250 255

Pro Lys Ala Gly Ala Val Asn Pro Thr Val Lys Phe Phe Val Val Asn
260 265 270

Thr Asp Ser Leu Ser Ser Val Thr Asn Ala Thr Ser Ile Gln Ile Thr
275 280 285

Ala Pro Ala Ser Met Leu Ile Gly Asp His Tyr Leu Cys Asp Val Thr

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290 295 300

Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln Trp Leu Arg Arg Ile Gln

305 310 315 320

Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr Asp Glu Ser Ser Gly Arg

325 330 335

Trp Asn Cys Leu Val Ala Arg Gln His Ile Glu Met Ser Thr Thr Gly

340 345 350

Trp Val Gly Arg Phe Arg Pro Ser Glu Pro His Phe Thr Leu Asp Gly

355 360 365

Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu Glu Gly Tyr Arg His Ile

370 375 380

Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys Thr Phe Ile Thr Lys Gly

385 390 395 400

Thr Trp Glu Val Ile Gly Ile Glu Ala Leu Thr Ser Asp Tyr Leu Tyr

405 410 415

Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro Gly Gly Arg Asn Leu Tyr

420 425 430

Lys Ile Gln Leu Ser Asp Tyr Thr Lys Val Thr Cys Leu Ser Cys Glu

435 440 445

Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser Val Ser Phe Ser Lys Glu

450 455 460

Ala Lys Tyr Tyr Gln Leu Arg Cys Ser Gly Pro Gly Leu Pro Leu Tyr

465 470 475 480

Thr Leu His Ser Ser Val Asn Asp Lys Gly Leu Arg Val Leu Glu Asp

485 490 495

Asn Ser Ala Leu Asp Lys Met Leu Gln Asn Val Gln Met Pro Ser Lys

500 505 510

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Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr Lys Phe Trp Tyr Gln Met
515 520 525

Ile Leu Pro Pro His Phe Asp Lys Ser Lys Lys Tyr Pro Leu Leu Leu
530 535 540

Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys Ala Asp Thr Val Phe Arg
545 550 555 560

Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr Glu Asn Ile Ile Val Ala
565 570 575

Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln Gly Asp Lys Ile Met His
580 585 590

Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu Val Glu Asp Gln Ile Glu
595 600 605

Ala Ala Arg Gln Phe Ser Lys Met Gly Phe Val Asp Asn Lys Arg Ile
610 615 620

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Thr Ser Met Val Leu
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Gly Ser Gly Ser Gly Val Phe Lys Cys Gly Ile Ala Val Ala Pro Val
645 650 655

Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr Thr Glu Arg Tyr Met Gly
660 665 670

Leu Pro Thr Pro Glu Asp Asn Leu Asp His Tyr Arg Asn Ser Thr Val
675 680 685

Met Ser Arg Ala Glu Asn Phe Lys Gln Val Glu Tyr Leu Leu Ile His
690 695 700

Gly Thr Ala Asp Asp Asn Val His Phe Gln Gln Ser Ala Gln Ile Ser
705 710 715 720

Lys Ala Leu Val Asp Val Gly Val Asp Phe Gln Ala Met Trp Tyr Thr

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725

730

735

Asp Glu Asp His Gly Ile Ala Ser Ser Thr Ala His Gln His Ile Tyr

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745

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Thr His Met Ser His Phe Ile Lys Gln Cys Phe Ser Leu Pro

755

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765